

SEQUENCE LISTING

<110> Madden, Mark
Weiner, David P.
Chaplin, Jennifer A.

<120> METHODS FOR PRODUCING ENANTIOMERICALLY PURE
ALPHA-SUBSTITUTED CARBOXYLIC ACIDS

<130> DIVER1440-2

<140> Not yet known

<141> 2000-12-28

<150> 60/254,414

<151> 2000-12-07

<150> 60/173,609

<151> 1999-12-29

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 1041

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Obtained from an
environmental sample

<220>

<221> CDS

<222> (1)..(1041)

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atg	tcg	gag	ccc	atg	acg	aag	tat	cgc	ggc	gcg	gcg	gtg	cag	gcc	gcg	48
Met	Ser	Glu	Pro	Met	Thr	Lys	Tyr	Arg	Gly	Ala	Ala	Val	Gln	Ala	Ala	
1				5				10					15			
ccg	gtg	ttc	ctc	gat	ctc	gac	cgc	aca	gtc	gag	aaa	gcg	atc	ggc	ctg	96
Pro	Val	Phe	Leu	Asp	Leu	Asp	Arg	Thr	Val	Glu	Lys	Ala	Ile	Gly	Leu	
			20				25						30			
atc	gag	cag	gcg	gcc	aag	cag	gac	gtg	cgc	ctg	atc	gca	ttc	cca	gag	144
Ile	Glu	Gln	Ala	Ala	Lys	Gln	Asp	Val	Arg	Leu	Ile	Ala	Phe	Pro	Glu	
		35					40					45				
act	tgg	att	ccc	ggc	tat	ccc	ttt	tgg	ata	tgg	ctg	ggc	gcg	ccg	gct	192
Thr	Trp	Ile	Pro	Gly	Tyr	Pro	Phe	Trp	Ile	Trp	Leu	Gly	Ala	Pro	Ala	
	50				55						60					
tgg	ggc	atg	cgc	ttc	gtc	cag	cgc	tat	ttc	gag	aat	tcg	ctc	gtg	cgc	240
Trp	Gly	Met	Arg	Phe	Val	Gln	Arg	Tyr	Phe	Glu	Asn	Ser	Leu	Val	Arg	
65					70				75						80	
ggc	agc	aag	cag	tgg	cag	gcc	ctg	gcg	gat	gcg	gcc	cgc	cgc	cac	ggc	288
Gly	Ser	Lys	Gln	Trp	Gln	Ala	Leu	Ala	Asp	Ala	Ala	Arg	Arg	His	Gly	
			85					90						95		
atg	cat	gtc	gtg	gcc	ggc	tat	agc	gag	cgc	gcg	ggc	ggc	agc	ctc	tat	336
Met	His	Val	Val	Ala	Gly	Tyr	Ser	Glu	Arg	Ala	Gly	Gly	Ser	Leu	Tyr	
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[illegible]

<213> Unknown Organism
 <223> Description of Unknown Organism: Obtained from an
 environmental sample

<400> 2

Met	Ser	Glu	Pro	Met	Thr	Lys	Tyr	Arg	Gly	Ala	Ala	Val	Gln	Ala	Ala		
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Pro	Val	Phe	Leu	Asp	Leu	Asp	Arg	Thr	Val	Glu	Lys	Ala	Ile	Gly	Leu		
			20					25					30				
Ile	Glu	Gln	Ala	Ala	Lys	Gln	Asp	Val	Arg	Leu	Ile	Ala	Phe	Pro	Glu		
		35					40					45					
Thr	Trp	Ile	Pro	Gly	Tyr	Pro	Phe	Trp	Ile	Trp	Leu	Gly	Ala	Pro	Ala		
	50					55					60						
Trp	Gly	Met	Arg	Phe	Val	Gln	Arg	Tyr	Phe	Glu	Asn	Ser	Leu	Val	Arg		
	65				70				75						80		
Gly	Ser	Lys	Gln	Trp	Gln	Ala	Leu	Ala	Asp	Ala	Ala	Arg	Arg	His	Gly		
			85						90					95			
Met	His	Val	Val	Ala	Gly	Tyr	Ser	Glu	Arg	Ala	Gly	Gly	Ser	Leu	Tyr		
			100					105					110				
Met	Gly	Gln	Ala	Ile	Phe	Gly	Pro	Asp	Gly	Asp	Leu	Ile	Ala	Ala	Arg		
		115					120					125					
Arg	Lys	Leu	Lys	Pro	Thr	His	Ala	Glu	Arg	Thr	Val	Phe	Gly	Glu	Gly		
	130					135					140						
Asp	Gly	Ser	His	Leu	Ala	Val	His	Asp	Thr	Ala	Ile	Gly	Arg	Leu	Gly		
	145				150					155					160		
Ala	Leu	Cys	Cys	Trp	Glu	His	Ile	Gln	Pro	Leu	Ser	Lys	Tyr	Ala	Met		
			165					170						175			
Tyr	Ala	Ala	Asp	Glu	Gln	Val	His	Val	Ala	Ser	Trp	Pro	Ser	Phe	Ser		
			180				185						190				
Leu	Tyr	Arg	Gly	Met	Ala	Tyr	Ala	Leu	Gly	Pro	Glu	Val	Asn	Thr	Ala		
		195					200					205					
Ala	Ser	Gln	Ile	Tyr	Ala	Val	Glu	Gly	Gly	Cys	Tyr	Val	Leu	Ala	Ser		
	210					215					220						
Cys	Ala	Thr	Val	Ser	Pro	Glu	Met	Ile	Lys	Val	Leu	Val	Asp	Thr	Pro		
	225				230				235						240		
Asp	Lys	Glu	Met	Phe	Leu	Lys	Ala	Gly	Gly	Gly	Phe	Ala	Met	Ile	Phe		
			245						250					255			
Gly	Pro	Asp	Gly	Arg	Ala	Leu	Ala	Glu	Pro	Leu	Pro	Glu	Thr	Glu	Glu		
		260						265					270				
Gly	Leu	Leu	Val	Ala	Asp	Ile	Asp	Leu	Gly	Met	Ile	Ala	Leu	Ala	Lys		
		275					280					285					
Ala	Ala	Ala	Asp	Pro	Ala	Gly	His	Tyr	Ser	Arg	Pro	Asp	Val	Thr	Arg		
		290				295					300						
Leu	Leu	Leu	Asp	Arg	Arg	Pro	Ala	Gln	Arg	Val	Val	Thr	Leu	Asp	Ala		
	305				310					315					320		
Ala	Phe	Glu	Pro	Gln	Asn	Glu	Asp	Lys	Gly	Asp	Ala	Pro	Ala	Leu	Arg		
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Val	Val	Ala	Glu	Ser	Ala	Ala	Ala	Ala	Gln								
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<210> 3
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 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Obtained from an
 environmental sample

<220>
 <221> CDS
 <222> (1)..(1014)

00951299.42000

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Met	Lys	Glu	Ala	Ile	Lys	Val	Ala	Cys	Val	Gln	Ala	Ala	Pro	Ile	Tyr		
1				5					10					15			
atg	gat	ttg	gag	gcg	acg	gtg	gac	aaa	acc	att	gag	ttg	atg	gaa	gaa	96	
Met	Asp	Leu	Glu	Ala	Thr	Val	Asp	Lys	Thr	Ile	Glu	Leu	Met	Glu	Glu		
		20						25					30				
gca	gca	cgt	aat	aat	gct	cgt	ctg	atc	gcc	ttt	ccg	gaa	act	tgg	att	144	
Ala	Ala	Arg	Asn	Asn	Ala	Arg	Leu	Ile	Ala	Phe	Pro	Glu	Thr	Trp	Ile		
		35					40					45					
cca	ggc	tac	cca	tgg	ttt	ctt	tgg	ctt	gac	tca	cca	gca	tgg	gca	atg	192	
Pro	Gly	Tyr	Pro	Trp	Phe	Leu	Trp	Leu	Asp	Ser	Pro	Ala	Trp	Ala	Met		
	50					55					60						
caa	ttt	gta	cgc	caa	tac	cat	gag	aac	tca	ttg	gag	ttg	gat	ggc	cct	240	
Gln	Phe	Val	Arg	Gln	Tyr	His	Glu	Asn	Ser	Leu	Glu	Leu	Asp	Gly	Pro		
65					70					75				80			
caa	gct	aag	cgc	att	tca	gat	gca	gcc	aag	cgg	ttg	gga	atc	atg	gtc	288	
Gln	Ala	Lys	Arg	Ile	Ser	Asp	Ala	Ala	Lys	Arg	Leu	Gly	Ile	Met	Val		
				85					90					95			
acc	ctg	ggg	atg	agt	gaa	cgg	gtc	ggg	ggc	acc	ctt	tac	atc	agt	cag	336	
Thr	Leu	Gly	Met	Ser	Glu	Arg	Val	Gly	Gly	Thr	Leu	Tyr	Ile	Ser	Gln		
			100					105					110				
tgg	ttc	ata	ggc	gat	aat	ggg	gac	acc	att	ggg	gcc	cgg	cga	aag	ttg	384	
Trp	Phe	Ile	Gly	Asp	Asn	Gly	Asp	Thr	Ile	Gly	Ala	Arg	Arg	Lys	Leu		
		115					120					125					
aaa	cct	act	ttt	gtt	gaa	cgt	act	ttg	ttc	ggc	gaa	ggg	gat	ggg	tca	432	
Lys	Pro	Thr	Phe	Val	Glu	Arg	Thr	Leu	Phe	Gly	Glu	Gly	Asp	Gly	Ser		
	130					135					140						
tcg	cta	gcg	gtt	ttc	gag	acg	tct	gtt	gga	agg	ctg	ggg	ggc	tta	tgc	480	
Ser	Leu	Ala	Val	Phe	Glu	Thr	Ser	Val	Gly	Arg	Leu	Gly	Gly	Leu	Cys		
145					150					155					160		
tgt	tgg	gag	cac	ctt	caa	ccg	cta	aca	aaa	tac	gct	ttg	tat	gca	caa	528	
Cys	Trp	Glu	His	Leu	Gln	Pro	Leu	Thr	Lys	Tyr	Ala	Leu	Tyr	Ala	Gln		
				165					170					175			
aat	gaa	gag	att	cat	tgt	gcg	gct	tgg	ccg	agc	ttt	agc	ctt	tat	cct	576	
Asn	Glu	Glu	Ile	His	Cys	Ala	Ala	Trp	Pro	Ser	Phe	Ser	Leu	Tyr	Pro		
			180					185					190				
aat	gcg	gcg	aaa	gcc	ctg	ggg	cct	gat	gtc	aat	gta	gcg	gcc	tct	cga	624	
Asn	Ala	Ala	Lys	Ala	Leu	Gly	Pro	Asp	Val	Asn	Val	Ala	Ala	Ser	Arg		
		195					200					205					
atc	tat	gcc	gtt	gaa	ggg	caa	tgc	ttc	gta	cta	gcg	tcg	tgt	gcg	ctc	672	
Ile	Tyr	Ala	Val	Glu	Gly	Gln	Cys	Phe	Val	Leu	Ala	Ser	Cys	Ala	Leu		
	210					215					220						
gtt	tca	caa	tcc	atg	atc	gat	atg	ctt	tgt	aca	gat	gac	gaa	aag	cat	720	
Val	Ser	Gln	Ser	Met	Ile	Asp	Met	Leu	Cys	Thr	Asp	Asp	Glu	Lys	His		
225					230					235					240		
gcg	ttg	ctt	ctg	gct	ggg	ggg	gga	cac	tca	cgt	atc	ata	ggg	cct	gat	768	
Ala	Leu	Leu	Leu	Ala	Gly	Gly	Gly	His	Ser	Arg	Ile	Ile	Gly	Pro	Asp		
				245					250					255			

ggt ggt gac ttg gtc gcg cct ctt gcc gaa aat gaa gag ggt att ctc	816
Gly Gly Asp Leu Val Ala Pro Leu Ala Glu Asn Glu Glu Gly Ile Leu	
260 265 270	
tac gca aac ctt gat cct gga gta cgc atc ctt gct aaa atg gcg gca	864
Tyr Ala Asn Leu Asp Pro Gly Val Arg Ile Leu Ala Lys Met Ala Ala	
275 280 285	
gac cct gct ggt cat tat tcc cgt ccc gac att act cgc ttg cta ata	912
Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Ile Thr Arg Leu Leu Ile	
290 295 300	
gat cgc agc cct aaa tta ccg gta gtt gaa att gaa ggt gat ctt cgt	960
Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg	
305 310 315 320	
cct tac gct ttg ggt aaa gcg tct gag acg ggt gcg caa ctc gaa gaa	1008
Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu	
325 330 335	
att tga	1014
Ile	

<210> 4
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 <212> PRT
 <213> Unknown Organism
 <223> Description of Unknown Organism: Obtained from an
 environmental sample

<400> 4

Met Lys Glu Ala Ile Lys Val Ala Cys Val Gln Ala Ala Pro Ile Tyr	
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Met Asp Leu Glu Ala Thr Val Asp Lys Thr Ile Glu Leu Met Glu Glu	
20 25 30	
Ala Ala Arg Asn Asn Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile	
35 40 45	
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Ala Met	
50 55 60	
Gln Phe Val Arg Gln Tyr His Glu Asn Ser Leu Glu Leu Asp Gly Pro	
65 70 75 80	
Gln Ala Lys Arg Ile Ser Asp Ala Ala Lys Arg Leu Gly Ile Met Val	
85 90 95	
Thr Leu Gly Met Ser Glu Arg Val Gly Gly Thr Leu Tyr Ile Ser Gln	
100 105 110	
Trp Phe Ile Gly Asp Asn Gly Asp Thr Ile Gly Ala Arg Arg Lys Leu	
115 120 125	
Lys Pro Thr Phe Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly Ser	
130 135 140	
Ser Leu Ala Val Phe Glu Thr Ser Val Gly Arg Leu Gly Gly Leu Cys	
145 150 155 160	
Cys Trp Glu His Leu Gln Pro Leu Thr Lys Tyr Ala Leu Tyr Ala Gln	
165 170 175	
Asn Glu Glu Ile His Cys Ala Ala Trp Pro Ser Phe Ser Leu Tyr Pro	
180 185 190	
Asn Ala Ala Lys Ala Leu Gly Pro Asp Val Asn Val Ala Ala Ser Arg	
195 200 205	
Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu	
210 215 220	
Val Ser Gln Ser Met Ile Asp Met Leu Cys Thr Asp Asp Glu Lys His	
225 230 235 240	
Ala Leu Leu Leu Ala Gly Gly Gly His Ser Arg Ile Ile Gly Pro Asp	
245 250 255	
Gly Gly Asp Leu Val Ala Pro Leu Ala Glu Asn Glu Glu Gly Ile Leu	

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